

**Amendments to Claims**

**Claims 1-2 (Canceled)**

**Claim 3 (Currently amended):** A method for generating a genome-registered collection of reporter gene fusions from an organism comprising the steps of:

- (a) generating a set of gene fusions comprising:
  - 1) a reporter gene or reporter gene complex operably linked to
  - 2) a genomic fragment from an organism of which at least 15% of the genomic nucleotide sequence is known;
- (b) introducing *in vitro* the reporter gene fusions from step (a) into a host organism;
- (c) registering the reporter gene fusions on the basis of sequence homology to the genomic sequence of the organism;
- (d) repeating (a), (b), and/or (c) until reporter gene fusions have been made to at least 15% of the known genomic nucleotide sequence of said organism.

**Claim 4 (Original):** A method according to Claim 3 wherein the gene fusions of step (a) are generated either *in vivo* or *in vitro*.

**Claim 5 (Currently amended):** The method of Claim 3 wherein: ~~A method for generating a genome-registered collection of reporter gene fusions comprising:~~

- (a) said generating a set of gene fusions comprises:
  - 1) generating random nucleic acid fragments from the DNA of an organism of which at least 15% of the nucleotide sequence is known; and
  - 2) operably linking the random nucleic acid fragments generated in (1a) to a vector containing a promoterless reporter gene or reporter gene complex in a vector; and
- (c) (b) said registering the reporter gene fusions on the basis of sequence homology to the genomic sequence of the organism of step (c) comprises ~~introducing the vector (b) containing the gene fusions into a host organism;~~
- (d) determining the nucleic acid sequence of the distal and the proximal ends of the random nucleic fragments relative to the reporter gene or reporter gene complex;
- (e) ~~registering the sequenced fusions of step (d) on the basis of sequence homology to the genomic sequence of the host organism;~~
- (d) ~~repeating (a), (b), and/or (c) until reporter gene fusions have been made to at least 15% of the known genomic nucleotide sequence of said organism~~

**Claim 6 (Currently amended):** A method according to Claim 5 wherein the random nucleic acid fragments of step (a) are generated by a method selected from the group consisting of restriction enzyme digestion, physical shearing of the genome and polymerase chain reaction.

**Claims 7-8 (Canceled)**

**Claim 9 (Currently amended):** A method according to ~~any one of~~ Claims 1, 3, or Claim 5, 7 or 8 wherein the organism is selected from the group consisting of prokaryotes and fungi.

**Claim 10 (Original):** A method according to Claim 9 wherein the prokaryote is an enteric bacterium.

**Claim 11 (Original):** A method according to Claim 10 wherein the enteric bacterium is selected from the group consisting of *Escherichia* and *Salmonella*.

**Claim 12 (Currently amended):** A method according to ~~one of~~ Claims 1, 3, or Claim 5, 7 ~~or 8~~ wherein the reporter gene or reporter gene complex is selected from the group consisting of *luxCDABE*, *lacZ*, *gfp*, *cat*, *galK*, *inaZ*, *luc*, *luxAB*, *bgaB*, *nptII*, *phoA*, *uidA* and *xylE*.

**Claim 13 (Currently amended):** A method according to ~~one of~~ Claims 1, 3, or Claim 5, 7 ~~or 8~~ wherein at least 50% of the genomic nucleotide sequence is known.

**Claims 14-22 (Canceled)**